

PCT09

#7

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/830,230

DATE: 11/14/2001

TIME: 14:14:48

Input Set : A:\PB481USsl.txt

Output Set: N:\CRF3\11142001\I830230.raw

2 <110> APPLICANT: Human Genome Sciences, Inc.
 4 <120> TITLE OF INVENTION: Lyme Disease Vaccines
 6 <130> FILE REFERENCE: PB481US
 8 <140> CURRENT APPLICATION NUMBER: 09/830,230
 9 <141> CURRENT FILING DATE: 2001-04-24
 11 <150> PRIOR APPLICATION NUMBER: PCT/US98/12718
 12 <151> PRIOR FILING DATE: 1998-06-18
 14 <150> PRIOR APPLICATION NUMBER: 60/057,483
 15 <151> PRIOR FILING DATE: 1997-09-03
 17 <150> PRIOR APPLICATION NUMBER: 60/053,344
 18 <151> PRIOR FILING DATE: 1997-07-22
 20 <150> PRIOR APPLICATION NUMBER: 60/053,377
 21 <151> PRIOR FILING DATE: 1997-07-22
 23 <150> PRIOR APPLICATION NUMBER: 60/050,359
 24 <151> PRIOR FILING DATE: 1997-06-20
 26 <160> NUMBER OF SEQ ID NOS: 756
 28 <170> SOFTWARE: PatentIn Ver. 2.0
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 31 <211> LENGTH: 216
 32 <212> TYPE: PRT
 33 <213> ORGANISM: Homo sapiens
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 37 1 5 10 15
 39 Ile Ile Tyr Val Phe Ser Tyr Pro Glu Ile Lys Asn Phe Ser Arg Gln
 40 20 25 30
 42 Asp Pro Val Phe Ser Asp Leu Lys Ile Lys Val Leu Lys Tyr Asn Lys
 43 35 40 45
 45 Lys Gln His Ile Pro Leu Phe Phe Tyr Ser Tyr Lys Val Lys Lys Gly
 46 50 55 60
 48 Asp Thr Phe Phe Lys Ile Ala Asn Lys Ile Asn Gly Trp Gln Ser Gly
 49 65 70 75 80
 51 Ile Ala Thr Ile Asn Leu Leu Asp Ser Pro Ala Val Ser Val Gly Gln
 52 85 90 95
 54 Glu Ile Leu Ile Pro Ser Lys Lys Gly Val Phe Val Phe Asp Ser Lys
 55 100 105 110
 57 Asp Tyr Arg Phe Asn Asn Leu Leu Leu Ala Thr Arg Asp Leu Ala Lys
 58 115 120 125
 60 Ala Glu Lys Val Lys Ile Lys Arg Asn Asp Arg Val Tyr Glu Phe Tyr
 61 130 135 140
 63 Phe Phe Asp Phe Val Lys Asn Pro Asp Phe Gly Leu Phe Ser Gly Thr
 64 145 150 155 160
 66 Glu Leu Leu Phe Phe Leu Asn Ala Asn Phe Ile Phe Pro Leu Lys Lys
 67 165 170 175
 69 Phe Ile Val Ser Ser Asp Phe Gly Phe Arg Asn Asp Pro Phe Thr Gly
 70 180 185 190
 72 Asn Lys Ser Phe His Thr Gly Ile Asp Leu Ala Ala Pro Met Asn Ala

ENTERED

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87 Asp Leu Lys Ile Lys Val Leu Lys Tyr Asn Lys Lys Gln His Ile Pro
88      20          25          30
90 Leu Phe Phe Tyr Ser Tyr Lys Val Lys Lys Gly Asp Thr Phe Phe Lys
91      35          40          45
93 Ile Ala Asn Lys Ile Asn Gly Trp Gln Ser Gly Ile Ala Thr Ile Asn
94      50          55          60
96 Leu Leu Asp Ser Pro Ala Val Ser Val Gly Gln Glu Ile Leu Ile Pro
97 65          70          75          80
99 Ser Lys Lys Gly Val Phe Val Phe Asp Ser Lys Asp Tyr Arg Phe Asn
100      85          90          95
102 Asn Leu Leu Leu Ala Thr Arg Asp Leu Ala Lys Ala Glu Lys Val Lys
103      100          105          110
105 Ile Lys Arg Asn Asp Arg Val Tyr Glu Phe Tyr Phe Phe Asp Phe Val
106      115          120          125
108 Lys Asn Pro Asp Phe Gly Leu Phe Ser Gly Thr Glu Leu Leu Phe Phe
109      130          135          140
111 Leu Asn Ala Asn Phe Ile Phe Pro Leu Lys Lys Phe Ile Val Ser Ser
112 145          150          155          160
114 Asp Phe Gly Phe Arg Asn Asp Pro Phe Thr Gly Asn Lys Ser Phe His
115      165          170          175
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118      180          185          190
120 Leu Leu Glu
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126 <213> ORGANISM: Homo sapiens
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130 ttttcttatac cagaaataaa aaattttctca aggcaagatc ctgttttttc tgatcttaaa 120
131 attaaagttt taaaatataa caaaaaacaa catattcctc tgttttttta ctcatataaa 180
132 gttaaaaaag gggatacttt ttttaaaatt gccataaaaa taaatggatg gcagtcgggc 240
133 attgctacta ttaattttatt agattctcct gctgtgagtg ttgggcaaga gattcttatt 300
134 cccagtaaaa aaggagtttt tgtttttgat agtaaagatt atagatttaa taatttgctt 360
135 ttagcaacaa gggatcttgc taaagctgaa aaggtaaaaa ttaaaaggaa cgacagagtt 420
136 tatgaatttt atttttttga ttttgtttaag aatccagatt ttggactttt ttcaggcaca 480
137 gaattgcttt ttttcttaaa tgccaatttt atttttcctt taaaaaaatt tattgttagt 540
138 tctgattttg gatttagaaa tgaccctttc actggcaaca aaagtttcca tacaggaata 600

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139 gatcttgcag ctccaatgaa tgctgaagtg tatcttcttc ttctggaata g          651
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144 <213> ORGANISM: Homo sapiens
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147 tcttatccag aaataaaaaa tttctcaagg caagatcctg ttttttctga tcttaaaatt 60
148 aaagtttttaa aatataacaa aaaacaacat attcctctgt ttttttactc atataaagtt 120
149 aaaaaaagggg atactttttt taaaattgcc aataaaataa atggatggca gtccggcatt 180
150 gctactatta atttattaga ttctcctgct gtgagtgttg ggcaagagat tcttattccc 240
151 agtaaaaaag gagtttttgt ttttgatagt aaagattata gatttaataa tttgctttta 300
152 gcaacaaggg atcttgctaa agctgaaaag gtaaaaatta aaaggaacga cagagtttat 360
153 gaatttttatt tttttgattt tgtaagaat ccagattttg gacttttttc aggcacagaa 420
154 ttgctttttt tcttaaatgc caattttatt tttcctttta aaaaatttat tgtagttct 480
155 gattttggat ttagaaatga ccctttcact ggcaacaaaa gtttccatac aggaatagat 540
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167 Tyr Cys Cys Thr Thr Ile Lys Ile Asn His Asp Tyr Glu Thr Asp Phe
168              20              25              30
170 Lys Val Leu Glu Ser Pro Ser Lys Tyr Ile Asn Ile Asp Val Ile Lys
171              35              40              45
173 Ala Thr Asn Glu Tyr Ile Tyr Ile Gln Ile Thr Asn Asn Ser Leu Asp
174   50              55              60
176 Val Val Lys Ile Asn Trp Gln Asn Thr Ser Leu Asn Asn Asp Lys Ile
177  65              70              75              80
179 Val Leu Lys Lys Glu Asp Leu Thr Ile Asn Asn Glu Thr Gly Tyr Lys
180              85              90              95
182 Asn Lys Tyr Arg Glu Phe Phe Ile Gly Pro Lys Thr Ser Phe Lys Phe
183              100             105             110
185 Lys Val Tyr Pro Leu Lys Ile His Ser Lys Asn Lys Asn Ser Asn Asn
186              115             120             125
188 Leu Ser Ser Thr Ile Lys Tyr Pro Ser Ile Phe Lys Leu Asn Ile Thr
189              130             135             140
191 Lys Val Gly Ile Glu Ala Lys Lys Thr Ile Asn Val Leu Ile Thr Arg
192 145             150             155             160
194 Thr Thr Lys Ile Asn Ile Thr Asn Lys
195              165
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198 <211> LENGTH: 152
199 <212> TYPE: PRT
200 <213> ORGANISM: Homo sapiens
202 <400> SEQUENCE: 6
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Input Set : A:\PB481USs1.txt

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204      1              5              10              15
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207              20              25              30
209 Thr Asn Glu Tyr Ile Tyr Ile Gln Ile Thr Asn Asn Ser Leu Asp Val
210              35              40              45
212 Val Lys Ile Asn Trp Gln Asn Thr Ser Leu Asn Asn Asp Lys Ile Val
213              50              55              60
215 Leu Lys Lys Glu Asp Leu Thr Ile Asn Asn Glu Thr Gly Tyr Lys Asn
216      65              70              75              80
218 Lys Tyr Arg Glu Phe Phe Ile Gly Pro Lys Thr Ser Phe Lys Phe Lys
219              85              90              95
221 Val Tyr Pro Leu Lys Ile His Ser Lys Asn Lys Asn Ser Asn Asn Leu
222              100             105             110
224 Ser Ser Thr Ile Lys Tyr Pro Ser Ile Phe Lys Leu Asn Ile Thr Lys
225              115             120             125
227 Val Gly Ile Glu Ala Lys Lys Thr Ile Asn Val Leu Ile Thr Arg Thr
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230 Thr Lys Ile Asn Ile Thr Asn Lys
231 145              150
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234 <211> LENGTH: 585
235 <212> TYPE: DNA
236 <213> ORGANISM: Homo sapiens
238 <400> SEQUENCE: 7
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240 ctaagtagaa atattgtcaa aaaatacata aaaacaatat ttctgatttc aatggtttat 120
241 ttttattggt gtacgacaat aaaaataaac catgattatg aaactgattt taaagttcta 180
242 gaatctccct ctaaatacat caatatagat gtaattaaag ctacaaatga atatatttat 240
243 attcaaatta caaacaatag cttagacgta gtaaaaaataa attggcaaaa cactagtctt 300
244 aacaacgata agatcgtctt aaaaaaagaa gatcttacaa taaacaatga aacagggtat 360
245 aaaaataaat acagagaggt ttttatttgt cctaaaactt catttaaat taaagtatat 420
246 ccactaaaaa ttcattctaa aaacaaaaat agcaataact taagctcaac tattaatat 480
247 ccgtctatct ttaagctcaa cataacaaaa gtaggaattg aagcaaaaaa aacaataaat 540
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253 <213> ORGANISM: Homo sapiens
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257 ccctctaaat acatcaatat agatgtaatt aaagctacaa atgaatatat ttatattcaa 120
258 attacaaaca atagcttaga cgtagtaaaa ataaattggc aaaacactag tcttaacaac 180
259 gataagatcg tcttaaaaaa agaagatctt acaataaaca atgaaacagg gtataaaaaat 240
260 aaatacagag agttttttat tggtcctaaa acttcattta aatttaaggt atatccacta 300
261 aaaattcatt ctaaaaacaa aaatagcaat aacttaagct caactattaa atatccgtct 360
262 atttttaagc tcaacataac aaaagtagga attgaagcaa aaaaaacaat aaatgtttta 420
263 ataacaagaa ctacaaaaat taatattact aataaatga 459
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266 <211> LENGTH: 1146

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267 <212> TYPE: PRT
268 <213> ORGANISM: Homo sapiens
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275           20           25           30
277 Asp Asp Glu Asn Ser Lys Lys Arg Asp Lys Leu Thr Leu Ser Gln Lys
278           35           40           45
280 Ser Tyr Leu Arg Glu Leu Glu Leu Ser Thr Asp Glu Asp Leu Lys Lys
281           50           55           60
283 Trp Ala Leu Lys Glu Gly Leu Lys Glu Thr Asp Val Ser Lys Ile Arg
284   65           70           75           80
286 Glu Leu Leu Leu Lys Lys Phe Gly Ile Asp Pro Glu Leu Phe Ile Lys
287           85           90           95
289 Gly Lys Gly Leu Ala Gly Ser Gly Arg Tyr Lys Ile Ile Ile Glu Thr
290           100          105          110
292 Ala Asp Asn Leu Glu Asn Phe Thr Tyr Gly Leu Thr Lys Asp Glu Ser
293           115          120          125
295 Ile Ile Phe Glu Gly Arg Val Asn Ile Leu Val Glu Asp Ile Lys Glu
296           130          135          140
298 Asn Lys Lys His Asn Ile Lys Gly Asp Arg Ile Val Leu Asn Lys Asn
299  145          150          155          160
301 Ser Lys Lys Leu Tyr Ala Ile Gly Asn Val Glu Tyr Ile Leu Asp Met
302           165          170          175
304 Asp Thr Asn Glu Lys Leu Tyr Phe Tyr Gly Asn Glu Phe Leu Val Asp
305           180          185          190
307 Phe Asp Ser Gln Asn Phe Leu Leu Lys Asn Gly Ile Leu Gln Lys Lys
308           195          200          205
310 Met Gln Lys Asn Gln Ile Asp His Ile Leu Ser Phe Gly Gly Lys Val
311           210          215          220
313 Leu Lys Lys Ile Asp Asn Asp Val Thr Ile Leu Glu Gln Ala Phe Ala
314  225          230          235          240
316 Thr Thr Ser Lys Ile Pro Glu Pro Tyr Tyr Ser Ile Lys Ala Ser Lys
317           245          250          255
319 Ile Trp Ala Leu Pro Ser Gly Asp Phe Gly Phe Leu Asn Ala Ile Phe
320           260          265          270
322 Tyr Met Gly Arg Val Pro Val Phe Tyr Ile Pro Phe Phe Phe Arg Pro
323           275          280          285
325 Gly Asp Ser Leu Phe Phe Asn Pro Ser Leu Gly Leu Asn Pro Arg Lys
326           290          295          300
328 Gly Phe Ser Val Phe Asn Thr Val Tyr Leu Phe Gly Asn Lys Ser Ser
329  305          310          315          320
331 Ser Glu Asp Ser Ser Phe Leu Asp Phe Asp Phe Asn Ser Val Tyr Asn
332           325          330          335
334 Ser Gly Lys Lys Pro Tyr Ile Arg Asn Gly Tyr Leu Thr Tyr Phe Phe
335           340          345          350
337 Ala Glu Asn Leu Ala Pro Ser Val Asn Lys Asp Tyr Val Lys Leu Ile
338           355          360          365

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Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/830,230

DATE: 11/14/2001

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Input Set : A:\PB481USs1.txt

Output Set: N:\CRF3\11142001\I830230.raw

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L:14335 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:322
L:14353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:322
L:24126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:545
L:24230 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:546
L:25101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:561
L:25166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:562
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